

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 30, 2002, 12:32:18 ; Search time 10 Seconds
(without alignments)
2086.259 Million cell updates/sec

Title: US-10-025-514-8

Perfect score: 2675

Sequence: 1 MSGKFRAGVCPKPKSAQCL.....IEQNTKSPLEMGKVNPTQK 503

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2052.5	76.7	418	1	ALAT_HUMAN
2	1909.5	71.4	409	1	ALAT_PAPAN
3	1508	56.4	421	1	ALAT_PIG
4	1500	56.1	412	1	ALAT_CALCIN
5	1467.5	54.9	411	1	ALAT_RAT
6	1465.5	54.8	416	1	ALAT_SHEEP
7	1447.5	54.1	413	1	ALAM_TAMSI
8	1447.5	54.1	416	1	ALAT_BOVIN
9	1403.5	52.5	413	1	ALST_TAMSI
10	1399.5	52.3	413	1	ALMS_TAMSI
11	1387.5	51.9	413	1	ALMS_TAMSI
12	1347	50.4	413	1	ALR1_MOUSE
13	1345	50.3	413	1	ALR2_MOUSE
14	1341	50.1	413	1	ALR3_MOUSE
15	1339.5	50.1	413	1	ALAF_RABIT
16	1332.5	49.8	413	1	ALAF_TAMSI
17	1328	49.6	413	1	ALR4_MOUSE
18	1319.5	49.3	413	1	ALR5_MOUSE
19	1306	48.8	412	1	ALAT_MUSCR
20	1293	48.3	405	1	ALAS_CAVPO
21	1266	47.3	403	1	ALAF_CAVPO
22	1246	46.6	410	1	COTR_CAVPO
23	1165	43.6	410	1	ALAT_DIDMA
24	1157.5	43.3	420	1	ALAU_HUMAN
25	850	31.8	423	1	AACT_HUMAN
26	829	31.0	418	1	COTR_MOUSE
27	820	30.7	405	1	CBG_HUMAN
28	819.5	30.6	406	1	CBG_SAISC
29	817.5	30.6	416	1	CPI1_RAT
30	816	30.5	406	1	IPSP_HUMAN
31	816	30.5	418	1	CPI6_RAT
32	816	30.5	427	1	KAIN_HUMAN
33	811	30.3	383	1	CBG_RABIT

34	805	30.1	430	1	CBG_SHEEP
35	804.5	30.1	417	1	KBP_MOUSE
36	804	30.1	412	1	THBG_PIG
37	804	30.1	412	1	THBG_SHEEP
38	803	30.0	413	1	CPI3_RAT
39	800	29.9	411	1	THBG_BOVIN
40	787.5	29.4	415	1	THBG_HUMAN
41	774.5	29.0	409	1	THBG_RAT
42	771.5	28.8	405	1	IPSP_MOUSE
43	771.5	28.8	418	1	SI24_APOSY
44	739	27.6	372	1	ALAT_CYPCA
45	720.5	26.9	397	1	CBG_MOUSE

ALIGNMENTS

RESULT 1
ALAT_HUMAN
ID ALAT_HUMAN STANDARD; PRT; 418 AA.
AC P01009; Q9P1P0; Q13672;
DT 21-JUL-1986 (Rel. 01. Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-1-
DE antiprotease) (PRO0684/PRO2209).
GN SERPINA1 OR PI OR AAT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=84107980; PubMed=6319097;
RX Bollen A., Herzog A., Cravador A., Herion P., Chuchana P.,
RA van der Straten A., Loriau R., Jacobs P., van Elsen A.;
RT "Cloning and expression in Escherichia coli of full-length
RT complementary DNA coding for human alpha 1-antitrypsin.";
RL DNA 2:255-264(1983).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=85036645; PubMed=6387509;
RA Rosenberg S., Barr P.J., Najarian R.C., Hallowell R.A.;
RT "Synthesis in yeast of a functional oxidation-resistant mutant of
RL human alpha-antitrypsin.";
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=85047190; PubMed=6093867;
RA Long G.L., Chandra T., Woo S.L.C., Davie E.W., Kurachi K.;
RT "Complete sequence of the cDNA for human alpha 1-antitrypsin and the
RL gene for the S variant.";
RN [4]
RP SEQUENCE FROM N.A., AND VARIANTS Z.
RX MEDLINE=87057257; PubMed=3491072;
RA Nukwa T., Satoh K., Brantly M.L., Ogushi F., Fells G.A.,
RT Courtney M., Crystal R.G.;
RT "Identification of a second mutation in the protein-coding sequence
RL of the Z type alpha 1-antitrypsin gene.";
RN [5]
RP J. Biol. Chem. 261:15989-15994(1986).
RN [6]
RP ERRATUM.
RA Nukwa T., Satoh K., Brantly M.L., Ogushi F., Fells G.A.,
RT Courtney M., Crystal R.G.;
RL J. Biol. Chem. 262:10412-10412(1987).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE=85176977; PubMed=2985281;
RA Ciliberto G., Dente L., Cortese R.;
RT "Cell-specific expression of a transfected human alpha 1-antitrypsin
RL gene.";
RL Cell 41:531-540(1985).

P49920	ovis aries
P29621	mus musculus
Q9tt35	sus scrofa
P50450	ovis aries
P05544	rattus norv
Q9tt36	bos taurus
P05543	homo sapien
P35577	rattus norv
P70438	mus musculus
Q60396	apodemus sy
P32759	cyprinus ca
Q06770	mus musculus

- RN [7] SEQUENCE FROM N.A.
RP TISSUE-Petal liver;
RC Zhang C., Yu Y., Zhang S., Ouyang S., Luo L., Wei H., Zhou G.,
RA Zhou W., Bi J., Zhang Y., Liu M., He F.;
RA "Functional prediction of the coding sequences of 32 new genes deduced
RT by analysis of cDNA clones from human fetal liver.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE OF 25-418.
RX MEDLINE=82220135; PubMed=7045697;
RA Carrell R.W., Jeppsson J.-O., Laurell C.-B., Brennan S.O., Owen M.C.,
RA Vaughan L., Boswell D.R.;
RA "Structure and variation of human alpha 1-antitrypsin.";
RL Nature 298:329-334(1982).
RN [9]
RP PRELIMINARY SEQUENCE OF 25-418.
RA Chan S.K.;
RT "The covalent structure of human alpha1-protease inhibitor.";
RL Fed. Proc. 41:1016-1016(1982).
RN [10]
RP SEQUENCE OF 1-67; 196-255 AND 387-418 FROM N.A.
RX MEDLINE=82220035; PubMed=6979715;
RA Leicht M., Long G.L., Chandra T., Kurachi K., Kidd V.J., Mace M. Jr.,
RA Davie E.W., Woo S.L.C.;
RT "Sequence homology and structural comparison between the chromosomal
RT human alpha 1-antitrypsin and chicken ovalbumin genes.";
RL Nature 297:655-659(1982).
RN [11]
RP SEQUENCE OF 291-418 FROM N.A.
RX MEDLINE=86005469; PubMed=3876243;
RA Riley J.H., Bathurst I.C., Edbrooke M.R., Carrell R.W., Craig R.K.;
RA "Alpha 1-antitrypsin and serum albumin mRNA accumulation in normal,
RT acute phase and Z2 human liver.";
RL FEBS Lett. 189:361-366(1985).
RN [12]
RP SEQUENCE OF 350-418 FROM N.A.
RX MEDLINE=82082539; PubMed=7031661;
RA Kurachi K., Chandra T., Friesner Degen S.J., White T.T.,
RA Marchloro T.I., Woo S.L.C., Davie E.W.;
RT "Cloning and sequence of cDNA coding for alpha 1-antitrypsin.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:6826-6830(1981).
RN [13]
RP SEQUENCE OF 387-418 FROM N.A.
RX MEDLINE=85225507; PubMed=3873938;
RA Coutelle C., Speer A., Rogers J., Kalsheker N., Humphries S.,
RA Williamson R.;
RT "Construction and partial characterization of a human liver cDNA
RL library.";
RN Biomed. Biochim. Acta 44:421-431(1985).
RN [14]
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RX MEDLINE=84292309; PubMed=6332197;
RA Loebermann H., Tokuka R., Deisenhofer J., Huber R.;
RT "Human alpha 1-proteinase inhibitor. Crystal structure analysis of
RT two crystal modifications, molecular model and preliminary analysis
RT of the implications for function.";
RL J. Mol. Biol. 177:531-556(1984).
RN [15]
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RX MEDLINE=89221004; PubMed=2785270;
RA Eng R., Loebermann H., Schneider M., Wiegand G., Huber R.,
RA Laurell C.-B.;
RT "The S variant of human alpha 1-antitrypsin, structure and
RT implications for function and metabolism.";
RL Protein Eng. 2:407-415(1989).
RN [16]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=20386623; PubMed=10933492;
RA Elliott P.R., Pei X.Y., Dafforn T.R., Lomas D.A.;
RT "Topography of a 2.0 A structure of alpha1-antitrypsin reveals targets
RT for rational drug design to prevent conformational disease.";
RL Protein Sci. 9:1274-1281(2000).
RN [17]
RP REVIEW.
RX MEDLINE=89352843; PubMed=2669992;
RA Kalsheker N.;
RT "Alpha 1-antitrypsin: structure, function and molecular biology of
RT the gene.";
RL Biosci. Rep. 9:129-138(1989).
RN [18]
RP REVIEW.
RX MEDLINE=91315455; PubMed=1859394;
RA Wu Y., Foreman R.C.;
RT "The molecular genetics of alpha 1 antitrypsin deficiency.";
RL Bioessays 13:163-169(1991).
RN [19]
RP VARIANT M2.
RX MEDLINE=88324438; PubMed=2901226;
RA Nukiwa T., Brantly M.L., Ogushi F., Fells G.A., Crystal R.G.;
RT "Characterization of the gene and protein of the common alpha 1-
RT antitrypsin normal M2 allele.";
RL Am. J. Hum. Genet. 43:322-330(1988).
RN [20]
RP VARIANT M3.
RX MEDLINE=90368097; PubMed=2394452;
RA Graham A., Hayes K., Weidinger S., Newton C.R., Markham A.F.,
RA Kalsheker N.A.;
RT "Characterisation of the alpha-1-antitrypsin M3 gene, a normal
RT variant.";
RL Hum. Genet. 85:381-382(1990).
RN [21]
RP VARIANT F.
RX MEDLINE=91241132; PubMed=2035534;
RA Okayama H., Brantly M., Holmes M., Crystal R.G.;
RT "Characterization of the molecular basis of the alpha 1-antitrypsin F
RT allele.";
RL Am. J. Hum. Genet. 48:1154-1158(1991).
RN [22]
RP VARIANT M-HEERLEN.
RX MEDLINE=89154435; PubMed=2784123;
RA Hofker M.H., Nukiwa T., van Paassen H.M.B., Neilen M., Kramps J.A.,
RA Klasen E.C., Frants R.R., Crystal R.G.;
RT "A Pro-->Leu substitution in codon 369 of the alpha-1-antitrypsin
RT deficiency variant PI M-Heerlen.";
RL Hum. Genet. 81:264-268(1989).
RN [23]
RP VARIANT M-MALTON.
RX MEDLINE=89270478; PubMed=2786335;
RA Fraizer G.C., Harrold T.R., Hofker M.H., Cox D.W.;
RT "In-frame single codon deletion in the M-Malton deficiency allele of
RT alpha 1-antitrypsin.";
RL Am. J. Hum. Genet. 44:894-902(1989).
RN [24]
RP VARIANT M-MINERAL SPRINGS.
RX MEDLINE=90097863; PubMed=1967187;
RA Curiel D.T., Vogelmeier C., Hubbard R.C., Stier L.E., Crystal R.G.;
RT "Molecular basis of alpha 1-antitrypsin deficiency and emphysema";
RT associated with the alpha 1-antitrypsin M-Mineral springs allele.";
RL Mol. Cell. Biol. 10:47-56(1990).
RN [25]
RP VARIANT M-NICHINAN.
RX MEDLINE=90178096; PubMed=2309708;
RA Matsunaga E., Shiohara S., Nakamura H., Maruyama T., Tsuda K.,
RA Fukumaki Y.;
RT "Molecular analysis of the gene of the alpha 1-antitrypsin deficiency
RT variant, M-Nichinan.";
RL Am. J. Hum. Genet. 46:602-612(1990).
RN [26]
RP VARIANT M-PROCIDA.
RX MEDLINE=89008457; PubMed=3262617;
RA Takahashi H., Nukiwa T., Satoh K., Ogushi F., Brantly M., Fells G.,
RA Stier L., Courtney M., Crystal R.G.;
RT "Characterization of the gene and protein of the alpha 1-antitrypsin
RT 'deficiency' allele M-Procida.";
RL J. Biol. Chem. 263:15528-15534(1988).

Query Match 76.7%; Score 2052.5; DB 1; Length 418;
 Best Local Similarity 97.8%; Pred. No. 5.7e-130;
 Matches 399; Conservative 2; Mismatches 4; Indels 3; Gaps 1;

QY 96 GMCCKSCVSPVKAMEDPQDAAQKTDTSHHDDHPTFNKIPNLAEFAFSLYROLAHOSN 155
 DB 14 GLC---CLVPVSLAEDPQDAAQKTDTSHHDDHPTFNKIPNLAEFAFSLYROLAHOSN 70
 QY 156 STNIFSPVSIATAFAMLSLGTADTHDEILGLNFTNTEPEAQIHGEGFQELLRLNQP 215
 DB 71 STNIFSPVSIATAFAMLSLGTADTHDEILGLNFTNTEPEAQIHGEGFQELLRLNQP 130
 QY 216 DSOLQLTGNGFLSEGLKLVDFKLEDKVLYHSEAFVNFCDTEAAKQINDYVEKGTQ 275
 DB 131 DSOLQLTGNGFLSEGLKLVDFKLEDKVLYHSEAFVNFCDTEAAKQINDYVEKGTQ 190
 QY 276 GKIVDLVKELDRDTVFALVNYIFFKQKWERPPEVKDTEEDPHVDQVTVTKVPMKRLGM 335
 DB 191 GKIVDLVKELDRDTVFALVNYIFFKQKWERPPEVKDTEEDPHVDQVTVTKVPMKRLGM 250
 QY 336 FNIOHCKLSSVLLMKYLGNTATAFFLPDEGKLOHLENELTHDIITKFLNEDRRSASL 395
 DB 251 FNIOHCKLSSVLLMKYLGNTATAFFLPDEGKLOHLENELTHDIITKFLNEDRRSASL 310
 QY 396 HLPKLSITGTYDLKSVLGOLGITKVFNSGADLSGVTEEAAPLKSKAVHKAVLTIDEGTE 455
 DB 311 HLPKLSITGTYDLKSVLGOLGITKVFNSGADLSGVTEEAAPLKSKAVHKAVLTIDEGTE 370
 QY 456 AGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLEMGKVVNPTQK 503
 DB 371 AGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLEMGKVVNPTQK 418

RESULT 2
 ALAT_PAPAN STANDARD; PRT; 409 AA.
 AC P01010;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-1-
 antiprotease) (AAT) (Fragment).
 GN SERPINAL OR PT.
 OS Papio anubis (Olive baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Papio.
 OX NCBI_TaxID=9555;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=82082539; PubMed=7031661;
 RA Kurachi K., Chandra T., Friesner Degen S.J., White T.T.,
 RT Marchioro T.B., Woo S.L.C., Davie E.W.;
 RT "Cloning and sequence of cDNA coding for alpha 1-antitrypsin.";
 RL Proc. Natl. Acad. Sci. U.S.A. 78:6826-6830(1981).
 CC -1- FUNCTION: INHIBITOR OF SERINE PROTEASES. ITS PRIMARY TARGET IS
 CC ELASTASE, BUT IT ALSO HAS A MODERATE AFFINITY FOR PLASMIN AND
 CC THROMBIN.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 CC -----
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 CC -----
 CC EMBL; J00321; AAA35377.1; -
 CC PIR; A01248; ITBA.

DR HSSP; P01009; 9API.
 DR InterPro; IPR000215; Serpin.
 DR Pfam; PF000079; serpin; 1.
 DR SMART; SM00093; SERPIN; 1.
 DR PROSITE; PS00284; SERPIN; 1.
 KW Serpin; serine protease inhibitor; Glycoprotein; Plasma; Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 15
 FT CHAIN 16 409
 FT ACT_SITE 373 374
 FT CARBOHYD 61 61
 FT CARBOHYD 98 98
 FT CARBOHYD 136 136
 FT CARBOHYD 262 262
 SQ SEQUENCE 409 AA; 45694 MW; E19B0B7450FDBA9B CRC64;

Query Match 71.4%; Score 1909.5; DB 1; Length 409;
 Best Local Similarity 90.2%; Pred. No. 2e-120;
 Matches 368; Conservative 21; Mismatches 16; Indels 3; Gaps 1;

QY 96 GMCCKSCVSPVKAMEDPQDAAQKTDTSHHDDHPTFNKIPNLAEFAFSLYROLAHOSN 155
 DB 5 GLC---CLLPGLSLAEDPQDAAQKTDTPHDQNHPTLNKIPSLAEFAFSLYROLAHOSN 61
 QY 156 STNIFSPVSIATAFAMLSLGTADTHDEILGLNFTNTEPEAQIHGEGFQELLRLNQP 215
 DB 62 STNIFSPVSIATAFAMLSLGTADTHDEILGLNFTNTEPEAQIHGEGFQELLRLNKP 121
 QY 216 DSOLQLTGNGFLSEGLKLVDFKLEDKVLYHSEAFVNFCDTEAAKQINDYVEKGTQ 275
 DB 122 DSOLQLTGNGFLSEGLKLVDFKLEDKVLYHSEAFVNFCDTEAAKQINDYVEKGTQ 181
 QY 276 GKIVDLVKELDRDTVFALVNYIFFKQKWERPPEVKDTEEDPHVDQVTVTKVPMKRLGM 335
 DB 182 GKIVDLVKELDRDTVFALVNYIFFKQKWERPPEVKDTEEDPHVDQVTVTKVPMKRLGM 241
 QY 336 FNIOHCKLSSVLLMKYLGNTATAFFLPDEGKLOHLENELTHDIITKFLNEDRRSASL 395
 DB 242 FNIOHCKLSSVLLMKYLGNTATAFFLPDEGKLOHLENELTHDIITKFLNEDRRSASL 301
 QY 396 HLPKLSITGTYDLKSVLGOLGITKVFNSGADLSGVTEEAAPLKSKAVHKAVLTIDEGTE 455
 DB 302 HLPKLSITGTYDLKSVLGOLGITKVFNSGADLSGVTEEAAPLKSKAVHKAVLTIDEGTE 361
 QY 456 AGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLEMGKVVNPTQK 503
 DB 362 AGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLEMGKVVNPTQK 409

RESULT 3
 ALAT_PIG STANDARD; PRT; 421 AA.
 AC P50447;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-1-
 antiprotease).
 GN SERPINAL OR PI.
 OS Sus scrofa (pig).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=97009792; PubMed=8856896;
 RA Archibald A.L., Couperwhite S., Mellink C.H.M., Lahbib-Mansais Y.,
 RT Gellin J.;
 RT "Porcine alpha-1-antitrypsin (PI): cDNA sequence, polymorphism and
 RT assignment to chromosome 7q2.4-q2.6".
 RL Anim. Genet. 27:85-89(1996).
 CC -1- FUNCTION: INHIBITOR OF SERINE PROTEASES. ITS PRIMARY TARGET IS

Mon Dec 9 12:51:04 2002

```

CC ELASTASE, BUT IT ALSO HAS A MODERATE AFFINITY FOR PLASMIN AND
CC THROMBIN (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
CC -----
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CC -----
CC EMBL; X88780; CAA61259.1; -.
CC HSP: P01009; 9API.
CC InterPro: IPR000215; Serpin.
CC Pfam: PF00079; serpin; 1.
CC SMART; SM00093; SERPIN; 1.
CC PROSITE; PS00284; SERPIN; 1.
CC Serpin; Serine protease inhibitor; Glycoprotein; Plasma; Signal.
CC FT SIGNAL 1 24
CC FT CHAIN 25 421
CC FT ACT_SITE 385 386
CC FT CARBOHYD 73 73
CC FT CARBOHYD 110 110
CC FT CARBOHYD 421 AA; 47194 MW; 08A4AB2A9E600690 CRC64;
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CC Query Match 56.4%; Score 1508; DB 1; Length 421;
CC Best Local Similarity 72.0%; Pred. No. 1.3e-93;
CC Matches 296; Conservative 40; Mismatches 69; Indels 6; Gaps 2;
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CC QY 96 GMGKSCVSPVKAMEPQGDAAQKDTSHDQD---HPTFNKITPNLAFAFSLYRQLAH 152
CC Db 14 GLC---CLVPISLAEGLOQHAVQETDVPDRHDEHQHQAACHRIAPNLADFAFSLYRQVAR 70
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CC QY 153 QSNSTNTFFSPVSTATAFAMLSLGTADHDEILEGLNLFNLTPEAQIHGEGFQELLRTL 212
CC Db 71 QSNSTNIFLSPVTARAFAMLSLGTGATHAEILEGLQFNLTKEAEIHGEGFQELLRTL 130
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CC QY 213 NQPSQQLTNGFLSEGLKLVDFKLEVDVKKLYHSEAFVNFVGTETEAKKQINDYVEK 272
CC Db 131 NQPSQQLTNGFLSEGLKLVDFKLEVDVKKLYHSEAFVNFVGTETEAKKQINDYVEK 190
CC
CC QY 273 GTQKIVDLVKELDRDVFALVNYIFFKQKWERPFVKTDEEDFHVDTTVTKVPMKMR 332
CC Db 191 GSQKIVDLVDLKDQTVFALVNYIFFKQKWERPFVKTDEEDFHVDTTVTKVPMKMR 250
CC
CC QY 333 LGMFNQICKLLSSWLLMKYLGNTATFFLPDEGKLOHLENELTHDIITKFLNEDRRS 392
CC Db 251 LGMFDLHCDLSSWLLMDYVATATAFFLIPDQGLKLOLEDMLTKEIRAKFLEKRYPS 310
CC
CC QY 393 ASLHLPKLSITGYDLKSVLGQGITTKVFSNGADLSGVTEAPLKLKSKAVHKAVLTIDEK 452
CC Db 311 ANLHLPKLSITGYDLKSVLGQGITTKVFSNGADLSGVTEAPLKLKSKALHRAVLTIDEK 370
CC
CC QY 453 GTEAAGFLEAIPMSIPPEVKFNKPFVFLMEQNTKSPLEPMGVNPTQ 503
CC Db 371 GTEATGATILEAIPMSIPPEVKFNKPFVFLMEQNTKSPLEPMGVNPTQ 421
CC
CC RESULT 4
CC ALAT_CALCN STANDARD; PRY; 412 AA.
CC ID ALAT_CALCN
CC AC O54763;
CC DT 15-JUN-2002 (Rel. 41, Created)
CC DT 15-JUN-2002 (Rel. 41, Last sequence update)
CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
CC DE Alpha-1-antitrypsin precursor (Alpha-1-antitrypsin) (Alpha-1-
CC proteinase inhibitor).
CC OS Callosciurus caniceps (Gray-bellied squirrel).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sclurognathi; Scluridae; Sciurinae;
CC Callosciurus.

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NCBI_TaxID=64664;
[1]
RN SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=98094263; PubMed=9434174;
RA Takamatsu N., Kojima M., Taniyama M., Ohba K., Uematsu T., Segawa C.,
RT Tsutou S., Watanabe M., Kondo J., Kondo N., Shiba T.;
RT "Expression of multiple alaphal-antitrypsin-like genes in hibernating
RT species of the squirrel family."
RL Gene 204:127-132(1997).
CC -1- FUNCTION: INHIBITOR OF SERINE PROTEASES (By similarity).
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB000552; BAA24422.1; -.
CC HSP: P01009; 9API.
CC InterPro: IPR000215; Serpin.
CC Pfam: PF00079; serpin; 1.
CC SMART; SM00093; SERPIN; 1.
CC PROSITE; PS00284; SERPIN; 1.
CC Serpin; Serine protease inhibitor; Glycoprotein; Plasma; Signal.
CC FT SIGNAL 1 24
CC FT CHAIN 25 412
CC FT ACT_SITE 377 378
CC FT CARBOHYD 65 65
CC FT CARBOHYD 102 102
CC FT CARBOHYD 165 165
CC FT CARBOHYD 266 266
CC FT CARBOHYD 412 AA; 45729 MW; 7235668E9E8FCC6 CRC64;
CC
CC Query Match 56.1%; Score 1500; DB 1; Length 412;
CC Best Local Similarity 71.0%; Pred. No. 4.4e-93;
CC Matches 289; Conservative 48; Mismatches 62; Indels 8; Gaps 2;
CC
CC QY 96 GMGKSCVSPVKAMEPQGDAAQKDTSHDQDHPFTFNKITPNLAFAFSLYRQLAHOSN 155
CC Db 14 GLC---CLAPGSLAGD---AQETDASKDDEHPACHAPNLAEAFADLYRVLARQSN 65
CC
CC QY 156 STNIFSPVSIATAFAMLSLGTADHDEILEGLNLFNLTPEAQIHGEGFQELLRLNOP 215
CC Db 66 TTNIFSPVSVATATAALSLGTGKDTHTQLEGLDFNLTEMAETDTHQGFQHLQLNRP 125
CC
CC QY 216 DSQQLTNGFLSEGLKLVDFKLEVDVKKLYHSEAFVNFVGTETEAKKQINDYVEKGTQ 275
CC Db 126 NNQQLTNGFLSEGLKLVDFKLEVDVKKLYHSEAFVNFVGTETEAKKQINDYVEKGTQ 185
CC
CC QY 276 GKIVDLVKELDRDVFALVNYIFFKQKWERPFVKTDEEDFHVDTTVTKVPMKRLGM 335
CC Db 186 GKIVDAVKTLDKNTVFALVNYIFFKQKWERPFVKTDEEDFHVDTTVTKVPMKRLGR 245
CC
CC QY 336 FNIQCKKLSWLLMKYLGNTATFFLPDEGKLOHLENELTHDIITKFLNEDRRSASL 395
CC Db 246 FDLLYCTTLASWVLDYLGNTATFFLPDEGKLOHLENELTHDIITKFLNEDRRSASL 305
CC
CC QY 396 HLPKLSITGYDLKSVLGQGITTKVFSNGADLSGVTEAPLKLKSKAVHKAVLTIDEKGT 455
CC Db 306 YFPKLSITGYDLKSVLGQGITTKVFSNGADLSGVTEAPLKLKSKAVHKAVLTIDEKGT 365
CC
CC QY 456 AAGAMFLEAIPMSIPPEVKFNKPFVFLMEQNTKSPLEPMGVNPTQ 502
CC Db 366 AAGVTVLEAIPMSIPPEVKFNKPFVFLMEQNTKSPLEPMGVNPTQ 412
CC
CC RESULT 5

```

Matches 278; Conservative 66; Mismatches 61; Indels 9; Gaps 3;

OY 89 RDLKCCMGCKSKCSPVKAMEDPQGDAACKTDTSHDDODHPTEKNITPNLAETAFSLYR 148
| | :| :||| ||| :||| ||| :||| :||| :||| :||| :||| :||| :|||
Db 7 RGILLALAC--CLAPSFLAED-----AQETDTSQDOOS-PTYRKISNLADFAFSLYR 57

OY 149 OLAHOSNTNIFFPVSIVATAPAMLSIGTKADPHDEILEGLNFNLTEIPEAQIHGFEQL 208
:|| :||||| :||||| :||||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 58 ELVHOSNTSNIFFPMSTITTAFAMLSLGSKGDRKQILGLEFNLTPQIPeADIHKAFHL 117

OY 209 LRTLNPQSOLQTGTNGLLVLDFEGLVDKFELDKYLHYSEAFVNVGCDTEBAKKOIND 268
|:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 118 LQTLNRPDSELQLTGNGLVFNNKLVEKELEEVKNYNTHSEAFSVNPADEEAKKVIN 177

OY 269 YVEKTQGIQVLDLVKELDRTVTVALNYVIFFKGKWPERFEVKDTEEBDFHVQDVTTVKVP 328
||||| :||||| :||||| :||||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 178 YVEKTQGIQVLDLMQJDEDTFVALNYVIFFKGKWRPENPEHTRDADFHVKSSTTVKVP 237

OY 329 MNKRGLGFNIHQCHKLSSWLLMKYLIGNATAIFFLPDGEKLOHLENLTHDIITKPLENE 308
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 238 MMNRLGFMHDHCYSTLSSWWMMDYLGUNATAIFFLPDDGKMHOLEQTLTKDLISRFLNR 297

OY 389 DRRSASUHLPKLSITCTYDLKSYGVGLQIKTVKFSAGDSLGVTEBAPLKLSKAHVAVLT 468
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 298 QTRSAILYFKPLSGTGYTNLTKLLSSLGITRVFNNDADLSGITEDAPLKLSQAHVAVLT 357

OY 449 IDEKGTAAACAMEFLAIPMSIPEVKEFKNPVFMLMEQONTKPSLFMKGKVNPQTQ 502
:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 358 LDERTGAAGTIVEAVPMSLPPOVKQRDPHFPIFMFIVESETQSPILFVGKVIDPTR 411

RESULT 6

ALAT_SHEEP STANDARD; PRT: 416 AA.

P12725;
01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
Alpha-1-antiproteiinase precursor (Alpha-1-antitrypsin) (Alpha-1-proteinase inhibitor).
Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Ovis.
NCBI_Taxid=9940;
[1]
SEQUENCE FROM N.A.
TISSUE=Liver;
MEDLINE=89366677; PubMed=2788872;
Brown W.M., Dziegielewska K.D., Foreman R.C., Saunders N.R., Wu Y.; "Nucleotide and deduced amino acid sequence of sheep alpha 1 antitrypsin";
Nucleic Acids Res. 17:6398-6398(1989).
[2]

SEQUENCE OF 25-55.
TISSUE=Plasma;
MEDLINE=G11144555; PubMed=1899999;
Mistry R., Snashall P.D., Totty N., Guz A., Tetley T.D.; "Isolation and characterization of sheep alpha 1-proteinase inhibitor";
Biochem. J. 273:685-690(1991).

-!- FUNCTION: INHIBITS HUMAN LEUKOCYTE ELASTASE, PIG PANCREATIC ELASTASE AND BOVINE TRYPSIN ON A 1:1 MOLAR BASIS.
-!- SUBCELLULAR LOCATION: Extracellular.
-!- TISSUE SPECIFICITY: PLASMA.
-!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.

RT RT
RL Gene 204:127-132(1997).
CC -!- TISSUE SPECIFICITY: EXPRESSED IN LIVER.
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY. HIGH, TO ALPHA-1-
CC ANTITRYPSIN.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AB000546; BAA24416.1; -
CC HSP: P01009; BAPI.
CC InterPro: IPR00215; Serpin.
CC Pfam: PF00079; serpin; 1.
CC SMART: SM00093; SERPIN; 1.
CC PROSITE: PS00284; SERPIN; 1.
CC Serpin; Serine protease inhibitor; Glycoprotein; Signal.
KW SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 413 ALPHA-1-ANTITRYPSIN-LIKE PROTEIN CM55-MM.
FT MOD_RES 25 25 PYRROLIDONE CARBOXYLIC ACID (POTENTIAL).
FT CARBOHYD 65 65 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 102 102 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 266 266 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT ACT_SITE 377 378 REACTIVE BOND (BY SIMILARITY).
SQ SEQUENCE 413 AA; 46212 MW; D1C37B899BB20B69 CRC64;

Query Match 54.1%; Score 1447.5; DB 1; Length 413;
Best Local Similarity 68.3%; Pred. No. 1.4e-89;
Matches 274; Conservative 60; Mismatches 62; Indels 5; Gaps 1;

QY 101 SCVSPVAMEDPQGAQKDTSHDDQDHTFNKPTNLAFAFSLYROLAHQSNSTNIF 160
DB 16 SCLGPGSLAQD-----AQETASKKQDEHSHAFHAEFALLSLYRLAHQSNSTNIF 70
QY 161 PPSVATAFAMLSLGTADTHDEILGFLNFTPEAQIHGFEQLLTLNQPDSLO 220
DB 71 PPSVATAFAMLSLGTADTHDEILGFLNFTPEAQIHGFEQLLTLNQPDSLO 130
QY 221 LTTGNGFLSLGKLVKDFLEDVKKLYHSEAFVNFQDTEAKKQINDYVEKGTQGI 280
DB 131 LTTGNGFLSIHQNLKLLDKFLEDVKKLYHSEALPTNFTTEARQOINSYVEKGTQGI 190
QY 281 LKVELDRDTFVALVNIFFKQKWERPEVDEEDFVQDVTTVKPMKRLGMFNIQH 340
DB 191 LKVELDRDTFVALVNIFFKQKWERPEVDEEDFVQDVTTVKPMKRLGMFNIQH 250
QY 341 CKKLSWLLMKYLGNAFAIFLDPDEGLQHLNETHDITKFELEDRSSASLHLPKL 400
DB 251 CSTLASWLVQMDYLGNAFAIFLDPDKQKQHLNETHDITKFELEDRSSASLHLPKL 310
QY 401 SITGYDLKSVLGOLGKTVFSGADLSGVTEAPKLKSAVHKAVLTIDEKGTAAAG 460
DB 311 SISGTYDLKSVLGOLGKTVFSGADLSGVTEAPKLKSAVHKAVLTIDEKGTAAAG 370

RESULT 8
ALAT_BOVIN STANDARD; PRT; 416 AA.
ID ALAT_BOVIN
AC P34955;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Alpha-1-antitrypsin precursor (Alpha-1-antitrypsin) (Alpha-1-

or send an email to license@isb-sib.ch).
CC EMBL: X15555; CAA33561.1; -
CC PIR: S05312; ITSH.
CC HSP: P01009; 1KCT.
CC InterPro: IPR00215; Serpin.
CC Pfam: PF00079; serpin; 1.
CC SMART: SM00093; SERPIN; 1.
CC PROSITE: PS00284; SERPIN; 1.
CC Serpin; Serine protease inhibitor; Glycoprotein; Plasma; Signal.
KW SIGNAL 1 24 ALPHA-1-ANTITRYPSIN-LIKE PROTEIN CM55-MM.
FT CHAIN 25 416 REACTIVE BOND.
FT ACT_SITE 380 381 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 269 269 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 39 39 A -> S (IN REF. 2).
FT CONFLICT 45 45 C -> A (IN REF. 2).
SQ SEQUENCE 416 AA; 45984 MW; 0B4702C0527321BF CRC64;

Query Match 54.8%; Score 1465.5; DB 1; Length 416;
Best Local Similarity 67.6%; Pred. No. 8.9e-91;
Matches 280; Conservative 62; Mismatches 67; Indels 5; Gaps 2;

QY 89 RDLKCCMGCKSCVSPVAMEDPQGAQKDTSHDDQDHTFNKPTNLAFAFSLYR 148
DB 7 RGLLLAALC---CLAPTSAGVLQGHAVQETDTHAQE--AACHKIAPLANFAFSIYH 61
QY 149 QLAHOSNTNIFPSPVATAFAMLSLGTADTHDEILGFLNFTPEAQIHGFEQL 208
DB 62 KLAHOSNTNIFPSPVATAFAMLSLGTADTHDEILGFLNFTPEAQIHGFEQL 121
QY 209 LRTLNQPSQLQTLTGNGFLSEGLKLVKDFLEDVKKLYHSEAFVNFQDTEAKKQIND 268
DB 122 LRTLNQPSQLQTLTGNGFLSEGLKLVKDFLEDVKKLYHSEAFVNFQDTEAKKQIND 181
QY 269 YVEKGTQGIKLVKDFLEDVKKLYHSEAFVNFQDTEAKKQINDYVEKGTQGI 328
DB 182 YVEKGTQGIKLVKDFLEDVKKLYHSEAFVNFQDTEAKKQINDYVEKGTQGI 241
QY 329 MKKRLGMFNIQHCKKLSWLLMKYLGNAFAIFLDPDEGLQHLNETHDITKFELE 388
DB 242 MNRLGMFNIQHCKKLSWLLMKYLGNAFAIFLDPDEGLQHLNETHDITKFELE 301
QY 389 DRRSASLHLPKLSTIGTVDLSVGLGKTVFSGADLSGVTEAPKLKSAVHKAVLT 448
DB 302 YASSANLHLPKLSTIGTVDLSVGLGKTVFSGADLSGVTEAPKLKSAVHKAVLT 361
QY 449 IDEKGTAAAGAFLEAIPMSIPPEVKENKPFVFLMIEONTKSPFLMGKVVNPTQ 502
DB 362 IDEKGTAAAGAFLEAIPMSIPPEVKENKPFVFLMIEONTKSPFLMGKVVNPTQ 415

RESULT 7
ALMM_TAMSI STANDARD; PRT; 413 AA.
ID ALMM_TAMSI
AC O54757;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alpha-1-antitrypsin-like protein CM55-MM precursor.
OS Tamias sibiricus (Siberian chipmunk) (Asian chipmunk).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Tamias.
NCBI_TaxID=64680;
RX [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA MEDLINE=98094263; PubMed=9434174;
RA Takamatsu N., Kojima M., Taniyama M., Ohba K., Uematsu T., Segawa C.,
RA Tsutou S., Watanabe M., Kondo J., Kondo N., Shiba T.;

191 LKELDRDVTALVNYIFFKGGKWKQPNNEQTRKDFHVDVETVVRVPMNRLGMFHLHH 250
 QY 341 CKKLSWVLLMKYLGKATFIFLDPDEKGLQHLNETHDITKFLNEDRRSASLHLPKL 400
 Db 251 CSTLASWVLMQYLGKATFIFLDPKGMQHLNETHDITKFLNEDRRSASLHLPKL 310
 QY 401 SITGTYDLKSVLGKATFIFLDPKGMQHLNETHDITKFLNEDRRSASLHLPKL 460
 Db 311 SITGTYDLKSVLGKATFIFLDPKGMQHLNETHDITKFLNEDRRSASLHLPKL 370
 QY 461 FLEAIPMSIPPEVKFNKPFVFLMEQNTKSPFLMGKVVNPQK 503
 Db 371 VLGNIRSLRYEIVDRPFLVVIYEHHTKSPFLMGKVVNPQK 413

RESULT 10
 ALMS_TAMSI STANDARD; PRT; 413 AA.
 ID ALSI_TAMSI
 AC O54760;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Alpha-1-antitrypsin-like protein CM55-SI precursor.
 OS Tamias sibiricus (Siberian chipmunk) (Asian chipmunk).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
 OC Tamias.
 OX NCBI_TaxID=64680;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=98094263; PubMed=9434174;
 RA Takamatsu N., Kojima M., Taniyama M., Ohba K., Uematsu T., Segawa C.,
 RA Tsutou S., Watanabe M., Kondo J., Kondo N., Shiba T.;
 RA "Expression of multiple alaphal-antitrypsin-like genes in hibernating
 RT species of the squirrel family."
 RL Gene 204:127-132(1997)
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN LIVER.
 CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY. HIGH, TO ALPHA-1-
 CC ANTITRYPSIN.
 CC
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 CC
 CC EMBL; AB000549; BAA24419.1; -.
 CC HSP; P01009; 9A1.
 CC InterPro: IPR000215; Serpin.
 CC Pfam: PF00079; serpin; 1.
 CC SMART; SM00093; SERPIN; 1.
 CC PROSITE; PS00284; SERPIN; 1.
 CC Serpin; Serine protease inhibitor; Glycoprotein; Signal.
 CC SIGNAL 1 24
 CC CHAIN 25 413
 CC MOD_RES 65 65
 CC CARBOHYD 102 102
 CC CARBOHYD 165 165
 CC CARBOHYD 266 266
 CC ACT_SITE 377 378
 CC REACTIVE_BOND (BY SIMILARITY).
 CC SEQUENCE 413 AA; 4620 MW; AB65A1D31B8CA2EC CRC64;
 Query Match 52.3%; Score 1399.5; DB 1; Length 413;
 Best Local Similarity 66.5%; Pred. No. 2.3e-86;
 Matches 268; Conservative 61; Mismatches 69; Indels 5; Gaps 1;
 QY 101 SCVSPVKAMEDPQGDAAQKTDTSHTDQHPFNKTNPLAEFAFSLYROLAHQSNSTNIF 160
 Db 16 SCLGPGSLAQD-----AQETASKQDQHPASHIAPLAFAEFSLYFVLARQSNSTNIF 70

161 FSPVSIATATFAMLSLGTAKADTHDEILEGLNFMNLTETPEAQIHEGQELRLTLNPDLSIQ 220
 Db 71 FSPVSIATATFAMLSLGTAKADTHDEILEGLNFMNLTETPEAQIHEGQELRLTLNPDLSIQ 130
 QY 221 LITGNGLFSEGLKLVDFKLEDEKLYHSEAFVFGDTEEAQKOLNDYVEKGTQCKIVD 280
 Db 131 LITGNGLFSEGLKLVDFKLEDEKLYHSEAFVFGDTEEAQKOLNDYVEKGTQCKIVD 190
 QY 281 LKELDRDVTALVNYIFFKGGKWKQPNNEQTRKDFHVDVETVVRVPMNRLGMFHLHH 340
 Db 191 LKELDRDVTALVNYIFFKGGKWKQPNNEQTRKDFHVDVETVVRVPMNRLGMFHLHH 250
 QY 341 CKKLSWVLLMKYLGKATFIFLDPDEKGLQHLNETHDITKFLNEDRRSASLHLPKL 400
 Db 251 CSTLASWVLMQYLGKATFIFLDPKGMQHLNETHDITKFLNEDRRSASLHLPKL 310
 QY 401 SITGTYDLKSVLGKATFIFLDPKGMQHLNETHDITKFLNEDRRSASLHLPKL 460
 Db 311 SITGTYDLKSVLGKATFIFLDPKGMQHLNETHDITKFLNEDRRSASLHLPKL 370
 QY 461 FLEAIPMSIPPEVKFNKPFVFLMEQNTKSPFLMGKVVNPQK 503
 Db 371 VLGNIRSLRYEIVDRPFLVVIYEHHTKSPFLMGKVVNPQK 413

RESULT 11
 ALMS_TAMSI STANDARD; PRT; 413 AA.
 ID ALMS_TAMSI
 AC O54758;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE Alpha-1-antitrypsin-like protein CM55-MS precursor.
 OS Tamias sibiricus (Siberian chipmunk) (Asian chipmunk).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
 OC Tamias.
 OX NCBI_TaxID=64680;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=98094263; PubMed=9434174;
 RA Takamatsu N., Kojima M., Taniyama M., Ohba K., Uematsu T., Segawa C.,
 RA Tsutou S., Watanabe M., Kondo J., Kondo N., Shiba T.;
 RA "Expression of multiple alaphal-antitrypsin-like genes in hibernating
 RT species of the squirrel family."
 RL Gene 204:127-132(1997)
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN LIVER.
 CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY. HIGH, TO ALPHA-1-
 CC ANTITRYPSIN.
 CC
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 CC
 CC EMBL; AB000547; BAA24417.1; -.
 CC HSP; P01009; 1QLP.
 CC InterPro: IPR000215; Serpin.
 CC Pfam: PF00079; serpin; 1.
 CC SMART; SM00093; SERPIN; 1.
 CC PROSITE; PS00284; SERPIN; 1.
 CC Serpin; Serine protease inhibitor; Glycoprotein; Signal.
 CC SIGNAL 1 24
 CC CHAIN 25 413
 CC MOD_RES 65 65
 CC CARBOHYD 102 102
 CC CARBOHYD 165 165
 CC ACT_SITE 377 378
 CC REACTIVE_BOND (BY SIMILARITY).
 CC SEQUENCE 413 AA; 4620 MW; AB65A1D31B8CA2EC CRC64;
 Query Match 52.3%; Score 1399.5; DB 1; Length 413;
 Best Local Similarity 66.5%; Pred. No. 2.3e-86;
 Matches 268; Conservative 61; Mismatches 69; Indels 5; Gaps 1;
 QY 101 SCVSPVKAMEDPQGDAAQKTDTSHTDQHPFNKTNPLAEFAFSLYROLAHQSNSTNIF 160
 Db 16 SCLGPGSLAQD-----AQETASKQDQHPASHIAPLAFAEFSLYFVLARQSNSTNIF 70

FT CARBOHYD 266 266 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ ACT_SITE 378 REACTIVE BOND (BY SIMILARITY).
 SEQUENCE 413 AA; 45952 MW; 430374CA26EBAF08 CRC64;

Query Match
 Best Local Similarity 51.9%; Score 1387.5; DB 1; Length 413;
 Matches 270; Conservative 55; Mismatches 73; Indels 5; Gaps 1;

QY 101 SCVSPVKAMEDPQGDAAQKTDTSHDDQHPFNKITPNLAEFAFSLYRLAHOSNSTNIF 160
 DB 16 SCILGPGSLAQD-----AQETASQDQHPASHRIAPLAEFALSRYLVAROSNTNIF 70

QY 161 FSPVSIATAFAMLSGKTADTHDEGLNLTPEAQIHGEGFQELLRTLNQPSQLQ 220
 DB 71 FSPVSIATAFAMLSGKTADTHDEGLNLTPEAQIHGEGFQELLRTLNQPSQLQ 130

QY 221 LTTGNGFLSEGLKLVDFLEKLVKLYHSEAFVNFQDTEEDPHVQVTVKVPKMLRGLM 280
 DB 131 LTTGNGFLSEGLKLVDFLEKLVKLYHSEAFVNFQDTEEDPHVQVTVKVPKMLRGLM 190

QY 281 LVKELDRDTFALVNYIFFKQKWERPEFVKDTEEDPHVQVTVKVPKMLRGLM 340
 DB 191 LVKELDRDTFALVNYIFFKQKWERPEFVKDTEEDPHVQVTVKVPKMLRGLM 250

QY 341 CKKLSWLLMKLYGNATATFFLPDEKGLQHLNELTHDITKFLNEDRRSASLHPLK 400
 DB 251 CKKLSWLLMKLYGNATATFFLPDEKGLQHLNELTHDITKFLNEDRRSASLHPLK 310

QY 401 SITGYDLKSLVGLGKITKVFNSGADLSGVTEAPLKLKAVKAVLTIDEKTEAGAM 460
 DB 311 SITGYDLKSLVGLGKITKVFNSGADLSGVTEAPLKLKAVKAVLTIDEKTEAGAM 370

QY 461 FLEAIPMSIPPEVKFNKPFVLMIEQNTKSPLFMGKVNPTQK 503
 DB 371 VGGITFMSRPKEVIFDRPFLVVIYHHTKSPLEFVGKVNPTQK 413

RESULT 12
 ID AIT1_MOUSE STANDARD; PRT: 413 AA.
 AC P07758;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alpha-1-antitrypsin 1-1 precursor (Serine protease inhibitor 1-1)
 GN (Alpha-1 protease inhibitor 1) (Alpha-1-antiprotease) (AAT).
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCBI_TaxID=10090;
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Liver;
 RX MEDLINE=92052104; PubMed=1946354;
 RA Borriello F., Krauter K.S.;
 RT "Multiple murine alpha 1-protease inhibitor genes show unusual
 evolutionary divergence";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:9417-9421(1991).
 RN [2]
 RP SEQUENCE OF 211-413 FROM N.A.
 RX MEDLINE=86163765; PubMed=3007061;
 RA Krauter K.S., Citron B.A., Hsu M.T., Powell D., Darnell J.E. Jr.;
 RT "Isolation and characterization of the alpha 1-antitrypsin gene of
 mice";
 RL DNA 5:29-36(1986).
 CC -1- FUNCTION: INHIBITOR OF SERINE PROTEASES. ITS PRIMARY TARGET IS
 CC ELASTASE, BUT IT ALSO HAS A MODERATE AFFINITY FOR PLASMIN AND
 CC THROMBIN.
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
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 CC -----

DR EMBL; M75721; AAC28869.1; -;
 DR EMBL; M12586; AAA51624.1; -;
 DR PIR; A25495; A25495;
 DR HSP; P01009; 8API;
 DR MGD; MGI:891971; Spil-1.
 DR InterPro; IPR000215; Serpin.
 DR Pfam; PF00079; serpin; 1.
 DR SMART; SM00093; SERPIN; 1.
 DR PROSITE; PS00284; SERPIN; 1.
 KW Serpin; Serine protease inhibitor; Glycoprotein; Plasma; Signal;
 FT Multigene family.
 FT SIGNAL 1 24 BY SIMILARITY.
 FT CHAIN 25 413 ALPHA-1-ANTITRYPSIN 1-1.
 FT ACT_SITE 377 378 REACTIVE BOND (BY SIMILARITY).
 FT CARBOHYD 64 64 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 101 101 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 265 265 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CONFLICT 246 246 H -> D (IN REF. 2).
 FT CONFLICT 323 323 P -> L (IN REF. 2).
 FT CONFLICT 404 404 L -> V (IN REF. 2).
 SQ SEQUENCE 413 AA; 46002 MW; 1124B2CC356232F4 CRC64;

Query Match 50.4%; Score 1347; DB 1; Length 413;
 Best Local Similarity 62.3%; Pred. No. 7.3e-83;
 Matches 255; Conservative 72; Mismatches 72; Indels 10; Gaps 4;

QY 96 GMDCKSCVSPVKAMEDPQGDAAQKTDTSHDDQHPFNKITPNLAEFAFSLYRLAHOSN 155
 DB 14 GLC---CLVPSFLAED-----VQETDTSQKQDS-PASHEIATNLDGFAISLYRELHOSN 64

QY 156 STNIFPSPVSIATAFAMLSGKTADTHDEGLNLTPEAQIHGEGFQELLRTLNQ 215
 DB 65 STNIFPSPVSIATAFAMLSGKTADTHDEGLNLTPEAQIHGEGFQELLRTLNQ 124

QY 216 DSOLQITGNGFLSEGLKLVDFLEKLVKLYHSEAFVNFQDTEEDPHVQVTVKVPKMLRGLM 275
 DB 125 DSOLQITGNGFLSEGLKLVDFLEKLVKLYHSEAFVNFQDTEEDPHVQVTVKVPKMLRGLM 184

QY 276 GKIVDLVKELDRDTFALVNYIFFKQKWERPEFVKDTEEDPHVQVTVKVPKMLRGLM 335
 DB 185 GKIVDLVKELDRDTFALVNYIFFKQKWERPEFVKDTEEDPHVQVTVKVPKMLRGLM 244

QY 336 FNIOHCCKLSSWLLMKLYGNATATFFLPDEKGLQHLNELTHDITKFLNEDRRSASL 395
 DB 245 LVHHCSTLSSWLLMKLYGNATATFFLPDEKGLQHLNELTHDITKFLNEDRRSASL 304

QY 396 HLPKLSITGYDLKSLVGLGKITKVFNSGADLSGVTEAPLKLKAVKAVLTIDEKGT 454
 DB 305 HLPKLSITGYDLKSLVGLGKITKVFNSGADLSGVTEAPLKLKAVKAVLTIDEKGT 364

QY 455 EAAGAMFLAEIPMSIPPEVKFNKPFVLMIEQNTKSPLFMGKVNPTQK 503
 DB 365 EAAGAMFLAEIPMSIPPEVKFNKPFVLMIEQNTKSPLFMGKVNPTQK 413

RESULT 13
 ID AIT2_MOUSE STANDARD; PRT: 413 AA.
 AC P22599; Q61283;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alpha-1-antitrypsin 1-2 precursor (Serine protease inhibitor 1-2)
 GN (Alpha-1 protease inhibitor 2) (Alpha-1-antiprotease) (AAT).
 OS SP1-2 OR AAT2.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=90152670; PubMed=2303252;
 RX Sifers R.N., Ledley F.D., Reed-Fourquet L., Ledbetter D.H.,
 RA Sifers R.N., Woo S.L.C.;
 RT "Complete cDNA sequence and chromosomal localization of mouse alpha
 RT 1-antitrypsin";
 RL Genomics 6:100-104 (1990).
 RN [2]
 RP SEQUENCE OF 12-413 FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Liver;
 RX MEDLINE=92052104; PubMed=1946354;
 RA Borriello F., Krauter K.S.;
 RT "Multiple murine alpha 1-protease inhibitor genes show unusual
 RT evolutionary divergence";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:9417-9421(1991).
 CC -1- FUNCTION: INHIBITOR OF SERINE PROTEASES. ITS PRIMARY TARGET IS
 CC ELASTASE, BUT IT ALSO HAS A MODERATE AFFINITY FOR PLASMIN AND
 CC THROMBIN.
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
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 CC -----
 CC EMBL; M25529; AAA37132.1; -;
 DR EMBL; M75716; AAC28865.1; -;
 DR HSP; P01009; 8API.
 DR MGD; MGI:891970; Spil-2.
 DR InterPro: IPR000215; Serpin.
 DR Pfam; PF00079; serpin; 1.
 DR SMART; SM00093; SERPIN; 1.
 DR PROSITE; PS00284; SERPIN; 1.
 DR Serpin; Serine protease inhibitor; Glycoprotein; Plasma; Signal;
 KW Multigene family.
 FT SIGNAL 1 24
 FT CHAIN 25 413
 FT ACT_SITE 377 378
 FT CARBOHYD 64 64
 FT CARBOHYD 101 101
 FT CARBOHYD 265 265
 FT CONFLICT 18 18
 FT CONFLICT 203 203
 FT CONFLICT 240 240
 FT CONFLICT 252 252
 FT CONFLICT 314 314
 FT CONFLICT 413 413
 FT SEQUENCE 413 AA; 49914 MW; D93B7B04E9446BC CRC64;
 SQ
 Query Match 50.3%; Score 1345; DB 1; Length 413;
 Best Local Similarity 62.6%; Pred. No. 9.9e-83;
 Matches 256; Conservative 71; Mismatches 72; Indels 10; Gaps 4;
 QY 96 GMCSCVSPVKAMEDPGDAAQKTDTHSHDQDHTFNKTPNLAFAFSLYRLAHQSN 155
 Db 14 GLC---CLVPSFLAED-----VQETDTSQKQDS-PASHEIATNLGDFALSILYRELVRQSN 64
 QY 156 STNIFSPVSIATAFAMLSLQKADTHDEILEGLNFNLNLTPEPAQIHGFGQELLRTINOP 215
 Db 65 TSNIFFSPVSIATAFAMLSLQKADTHDEILEGLNFNLNLTPEPAQIHGFGQELLRTINOP 124
 QY 216 DSOLQLTGNGFLSEGLKLVDFKLEEDVYKLYHSEAFVNFQDTEEAQKQINDYVEKGTQ 275
 Db 125 DSELQLTGNGFLVNDKLVKFELEAKNHYQAEVSVNFAESEAKKVINDPVEKGTQ 184
 QY 276 GKIVDLVKELDRQTVFALVNIFFKQKWERPEVFKDTEEDFHVQDQVTVKVPMMKRLGM 335
 Db 185 GKIVEAVKELDQTVFALVNIFFKQKWERPEVFKDTEEDFHVQDQVTVKVPMMKRLGM 244

QY 336 FNIOHCKLLSWLLMKYLGNATIAIFFLPDEGKLOHLENELTHDIITKPLENEDRRSASL 395
 Db 245 LDVHHCSTLSSWLLMDYAGNASAVELLPEQKMQHLEQTLNKLKELISKILLNRRRLVQI 304
 QY 396 HLPKLSTGTGYDLKSVLQGLGKTVFSNGADLSGVTEE-APLKLSKAVHKAVLTIDEXGT 454
 Db 305 HIPRLSISGEVNLKLTSPILGTRIFNNGADLSGVTEENAPLKLSKAVHKAVLTIDETGT 364
 QY 455 BAAGAMFLEAIPSPPEVKFNKPFVFLMTEQNTKSPLFMGKVVNPQK 503
 Db 365 EAAATVFEAVPMSPILRDPHFLEIIEEHTQSPFVGVKVDPTHK 413
 RESULT 14
 ALT3_MOUSE STANDARD; PRT; 413 AA.
 ID AC Q00896;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alpha-1-antitrypsin 1-3 precursor (Serine protease inhibitor 1-3)
 DE (Alpha-1 protease inhibitor 3).
 GN Spil-3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Liver;
 RX MEDLINE=92052104; PubMed=1946354;
 RA Borriello F., Krauter K.S.;
 RT "Multiple murine alpha 1-protease inhibitor genes show unusual
 RT evolutionary divergence";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:9417-9421(1991).
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 CC -----
 CC EMBL; M75720; AAC28868.1; -;
 DR HSP; P01009; 9API.
 DR MGD; MGI:891969; Spil-3.
 DR InterPro: IPR000215; Serpin.
 DR Pfam; PF00079; serpin; 1.
 DR SMART; SM00093; SERPIN; 1.
 DR PROSITE; PS00284; SERPIN; 1.
 DR Serpin; Serine protease inhibitor; Glycoprotein; Plasma; Signal;
 KW Multigene family.
 FT SIGNAL 1 24
 FT CHAIN 25 413
 FT ACT_SITE 377 378
 FT CARBOHYD 64 64
 FT CARBOHYD 101 101
 FT CARBOHYD 265 265
 FT SEQUENCE 413 AA; 49854 MW; 7EAD710919A1C5B CRC64;
 SQ
 Query Match 50.1%; Score 1341; DB 1; Length 413;
 Best Local Similarity 62.6%; Pred. No. 1.8e-82;
 Matches 256; Conservative 70; Mismatches 73; Indels 10; Gaps 4;
 QY 96 GMCSCVSPVKAMEDPGDAAQKTDTHSHDQDHTFNKTPNLAFAFSLYRLAHQSN 155
 Db 14 GLC---CLVPSFLAED-----VQETDTSQKQDS-PASHEIATNLGDFALSILYRELVRQSN 64

